

MRALEGPGLSLILCLVLALPALLPVPVAVRGVAETPTYPWDAETGERLVCAQCPCPGTFVQR  
PCRRDSPPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF  
AHAGFCLEHASCPGAGVIAPGTPSQNTQCQPCPPGTFSSSSSSSEQCQPHRNCTALGLA  
LNVPGSSSHDTLCTSTCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLOALEAPE  
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLALRVARMPGLERSVRERFLPVH

## FIG. 1

TCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTGCGGTGAGGCACAGCAGGGTCCTGT  
GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC  
><Met {trans-1-s, dir=f, res=1}>  
ATGAGGCGCTGGAGGGGCCAGGCCTGTGCTGCTGTGCCTGGTGTGGCGCTGCCTGCC  
CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC  
GCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACCTTTGTGCAGCGG  
CCGTGCCGCGGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG  
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG  
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC  
GCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC  
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCC  
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC  
CTCAATGTGCCAGGCTCTTCCTCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC  
CTCAGCACCAGGCTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTGATCGACTTTGTGGCT  
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGAG  
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGACGCTGAAGCTGCGTCCGGCGG  
CTCACGGAGCTCTGGGGGCGCAGGACGGGGCGCTGCTGGTGGCGCTGCTGCAGGCGCTG  
CGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCTGTGCAC  
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCCACTTGCACTGAAAGAGG  
CTTTTTTTTAAATAAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

## FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCTCTGNNG  
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT  
GCCGCTGCCGACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC  
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA  
GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
GGCCCTCAATGTGCCAGGCTCTTCCTCCATGACACCCTGTGCACCAGCT  
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG  
CGTGCCGTGATCGACTTTGTGGCTTTCAGGACATCTCCAT

## FIG. 3

SEQ ID NO:4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
SEQ ID NO:5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACG  
SEQ ID NO:6 1 G  
SEQ ID NO:3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG

SEQ ID NO:4 178 CA-TTCTGGAACCTACCTGGAGCGC  
SEQ ID NO:5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCTCTGNGG  
SEQ ID NO:6 2 CAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGG  
SEQ ID NO:3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCTCTGNGG

SEQ ID NO:5 101 GGAGCNTGAGGAGGAGGCGANGNGCTTGCCACGCCACCCACAACCGCGCCT  
SEQ ID NO:6 52 GGAGCGTGAGGAGGAGGCGACGGGCTTGCCACGCCACCCACAACCGTGCCT  
SEQ ID NO:7 1 GAGGGGCCCCCAGGAGTGGTGGCCGAGGTG  
SEQ ID NO:3 101 GGAGCGTGAGGAGGAGGCGACGGGCTTGCCACGCCACCCACAACCGTGCCT

SEQ ID NO:5 151 GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNTTCTGCTTGAGGCAC  
SEQ ID NO:6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGGCAC  
SEQ ID NO:7 32 TGGCAGGGGTGAGGTTGCTGGTCCAGCCTTGACCCCTGAGCTAGGACAC  
SEQ ID NO:3 151 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGGCAC

SEQ ID NO:5 201 GCATCGTGTCCACCTGGTGCGGGCGTGATTGCNCCGGGCACCCCCAGCCA  
SEQ ID NO:6 152 GCATCGTGTCCACCTGGTGCGGGCGTGATTNCCCCGGGCACCCCCAGCCA  
SEQ ID NO:7 82 CAGTTCCCCTGACCCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA  
SEQ ID NO:8 1 GCATCGTGTCCACCTGGTGCGGGCGTGATTGCCCCGGGCACCCCCAGCCA  
SEQ ID NO:10 1 CTTGTCCACCTGGTGCGGGCGTGATTNCCC-GGGCACCCCCAGCCA  
SEQ ID NO:3 201 GCATCGTGTCCACCTGGTGCGGGCGTGATTGCCCCGGGCACCCCCAGCCA

SEQ ID NO:5 251 GAACACGCA-TGCAAAGCCGTG  
SEQ ID NO:7 132 GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
SEQ ID NO:8 51 GAACACGCAG-GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
SEQ ID NO:10 47 GAACACGCAGTGCC-AGCCNT-CCCCCAGGCACCTTCTCAGCCAGCAGC  
SEQ ID NO:9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT  
SEQ ID NO:3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC

SEQ ID NO:7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
SEQ ID NO:8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
SEQ ID NO:10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGNC-T  
SEQ ID NO:9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
SEQ ID NO:3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT

SEQ ID NO:7 232 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAG  
SEQ ID NO:8 151 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT  
SEQ ID NO:10 147 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT  
SEQ ID NO:9 86 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACAGCTGTGCACCAGCT  
SEQ ID NO:3 351 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT

SEQ ID NO:10 197 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG  
SEQ ID NO:9 136 GCACTGGCTTCCCCCTCAGCACCAGGGTANCAGGAGCTGAGGAGTGTGAG  
SEQ ID NO:3 401 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG

SEQ ID NO:10 247 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT  
SEQ ID NO:9 186 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT  
SEQ ID NO:3 451 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

FIG. 4

DNA30942 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A E T P T Y P W R D . A E T G  
htnfr2 1 M A P V A V W A A L A V G L E L W A A A H A L P A Q V A F T P V . A P E P G S T C R L R E Y Y D Q T

DNA30942 45 E R L V C A Q C P P G T F V Q R P C R R D S P T T C G P C P P R R H Y T Q F W N Y L E R C R Y C N V L  
htnfr2 50 A Q M C C S K C S P G Q H A K V F C T K T S D T V C D S C E D S T Y T Q L W N W V P E C L S C G S R

DNA30942 95 C G E R E E A R A C H A T H N R A C R C R T G F F . . . A H A G . . F C L E H A S C P P G A G V  
htnfr2 100 C S S D Q V E T Q A C T R E Q N R I C T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G F G V

DNA30942 139 I A P G T P S Q N T O C Q P C P P G T P S A S S S S E Q C Q P H R N C T A L G L A L N V P G S S S  
htnfr2 150 A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C R P H Q I C N V V A . . . I P G N A S

DNA30942 189 H D T L C T S C T G F P L S T R V P G A E E C E R A V I D F V A F Q D I S I K R L Q R L L Q A L E A  
htnfr2 196 R D A V C T S T S . . P T R S M A P G A V H L P Q P V S T R S Q H T Q P T P E P S T A P S T S F L L

DNA30942 239 P E G W G P T P . . R A G R A A L Q L K L R R R L T E L L G A Q D G A L L V R R L L Q A L R V A R M P  
htnfr2 244 P M G P S P P A E G S T G D P A L P V G L I V G V T A L G L L I I G V V N C V I M T Q V K K P L .

DNA30942 287 G L E R S V R E R F L P V H  
htnfr2 293 C L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S S S L E S S A S A L D R R A

htnfr2 343 P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C I V N V C S S S D

htnfr2 393 H S S Q C S S Q A S S T M G D T D S S P S E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G

htnfr2 443 S T E E K P L P L G V P D A G M K P S

FIG.5

DcR3 1 M R A L E G P G L S L C L V L A L P A L L P V P A V R G V A 31  
OPG 1 M N K L L C C A L V F L D L S I K W T T Q E T F P - - - - 25

CRD1

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T P V Q R P C 62  
OPG 26 - - P K Y L H Y D E E T S H Q L L C D K K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R R H Y T Q P W N Y L E R C R Y C N V 93  
OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD2

DcR3 94 L C G E R E E E A R A C H A T H N R A C R T G F F A H A G 124  
OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155  
OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4

DcR3 156 G T F B A S S S E Q C Q P H R N C T A L G L A L N V P G S 186  
OPG 148 G F F S N B T S S K A P C R K H T N C S V F G L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217  
OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247  
OPG 209 E A V P T X F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277  
OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S S V R E R F L P V H 300  
OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

FIG. 6

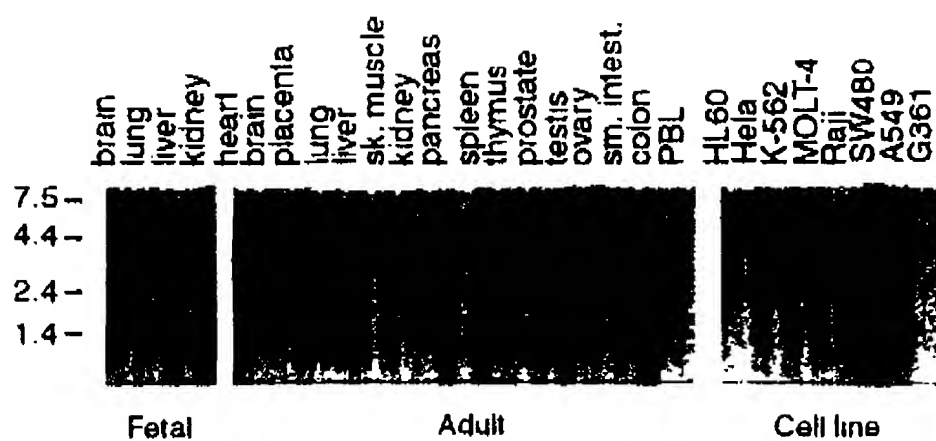
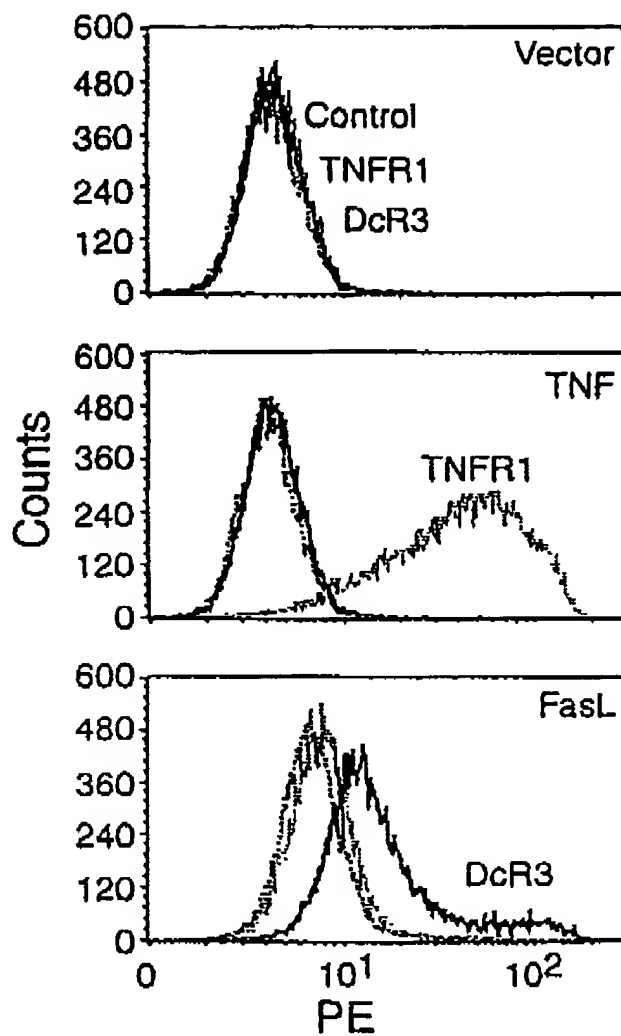
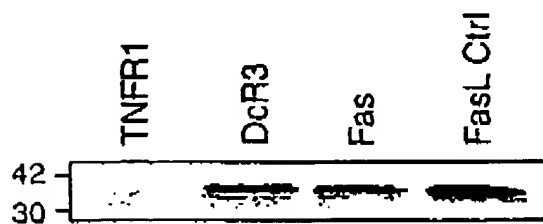


FIG. 7



**FIG. 8A**



**FIG. 8B**

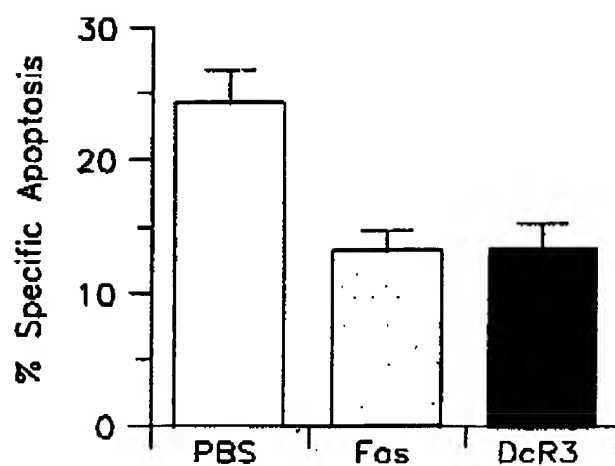


FIG. 9A

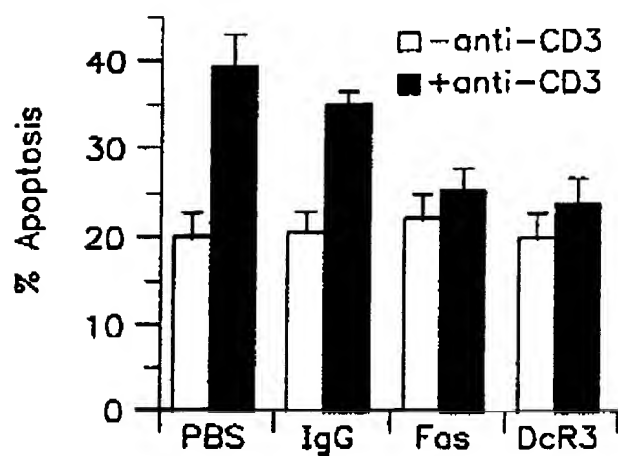


FIG. 9B

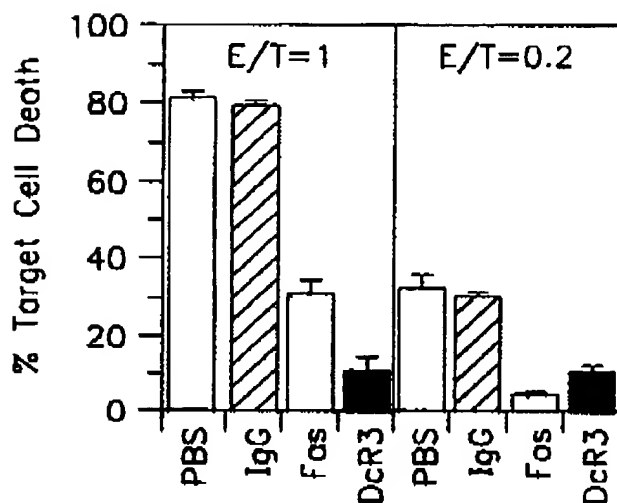
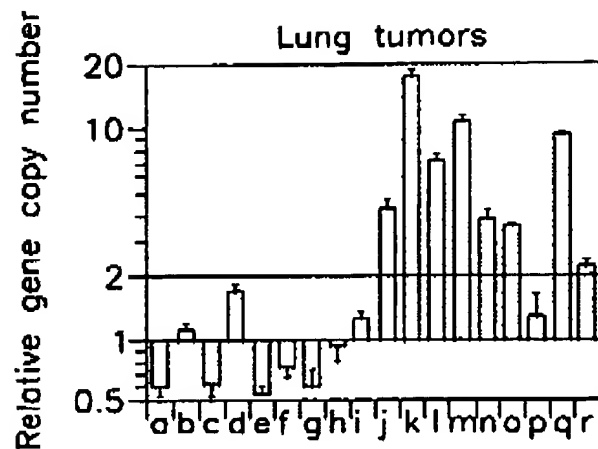
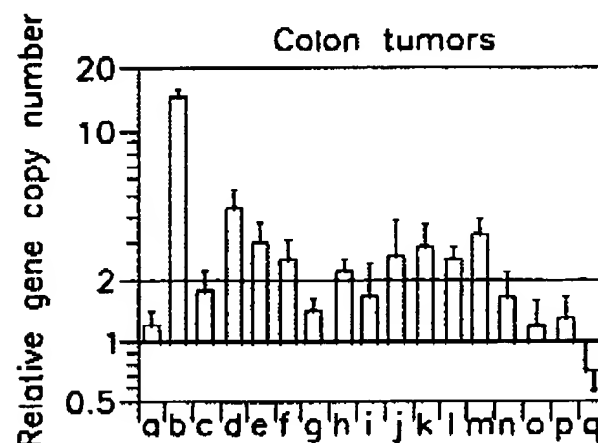


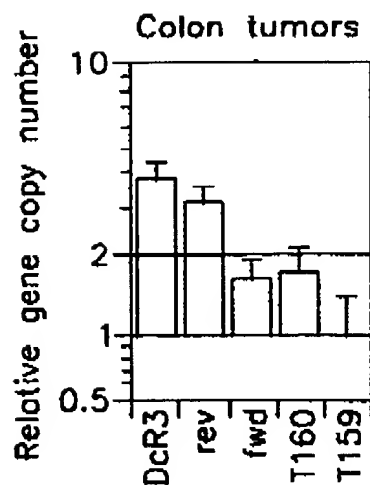
FIG. 9C



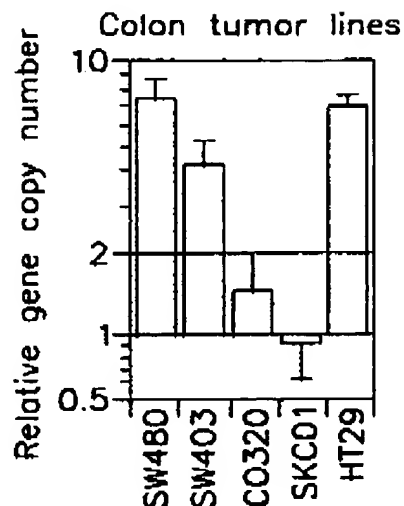
**FIG. IOA**



**FIG. IOB**



**FIG. IOC**



**FIG. IOD**



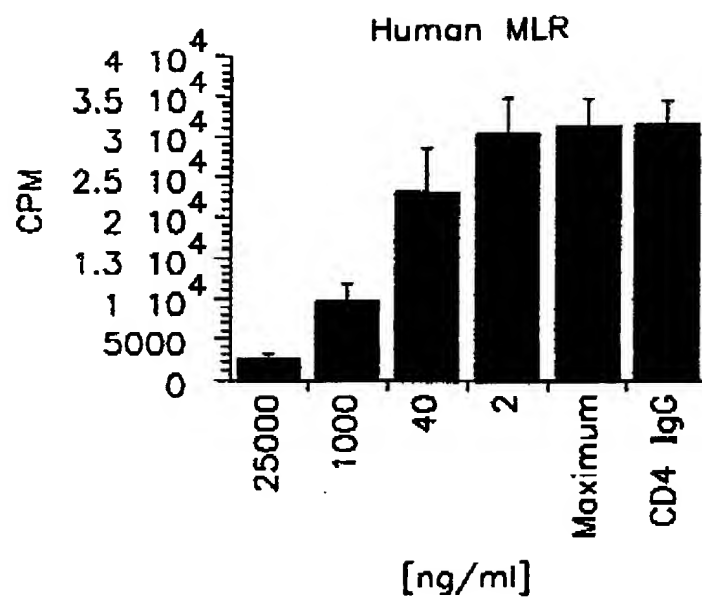


FIG. 1 IA

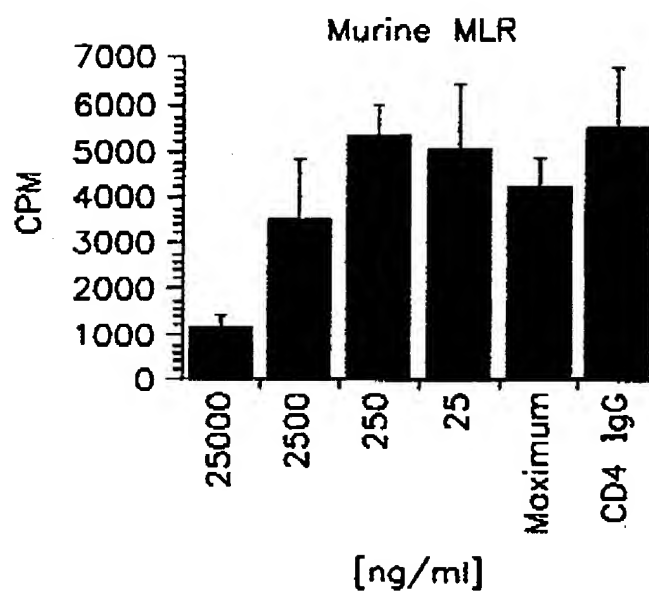


FIG. 1 IB

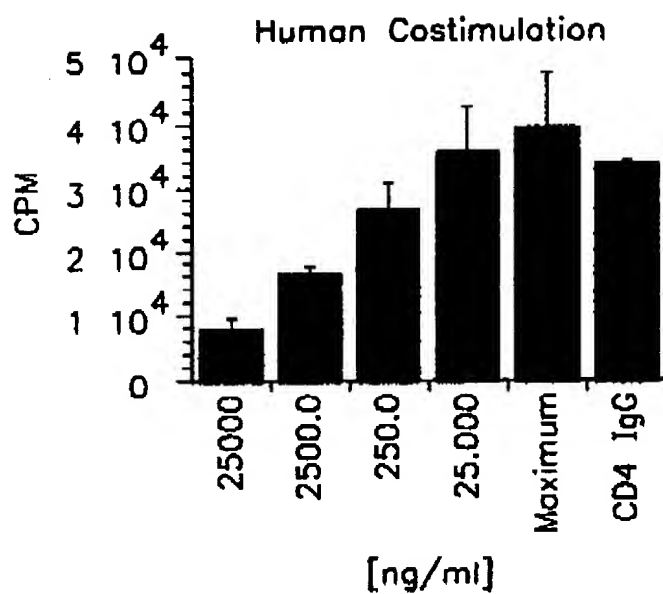


FIG. 1 IC

mAb	Isotype	Antigen Specificity (ELISA)				% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1 OPG	
4B7.1.1	IgG1	+++	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.  
 % blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

**FIG. 12**

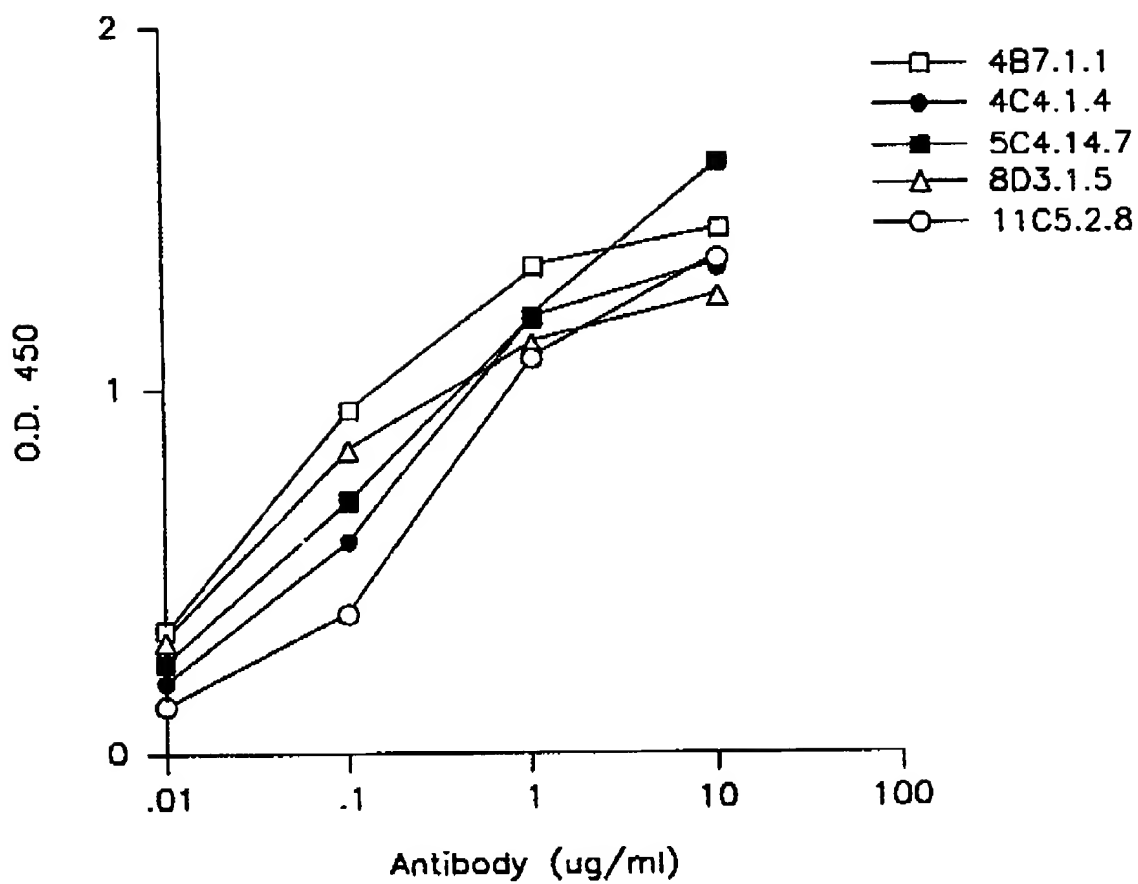


FIG. 13

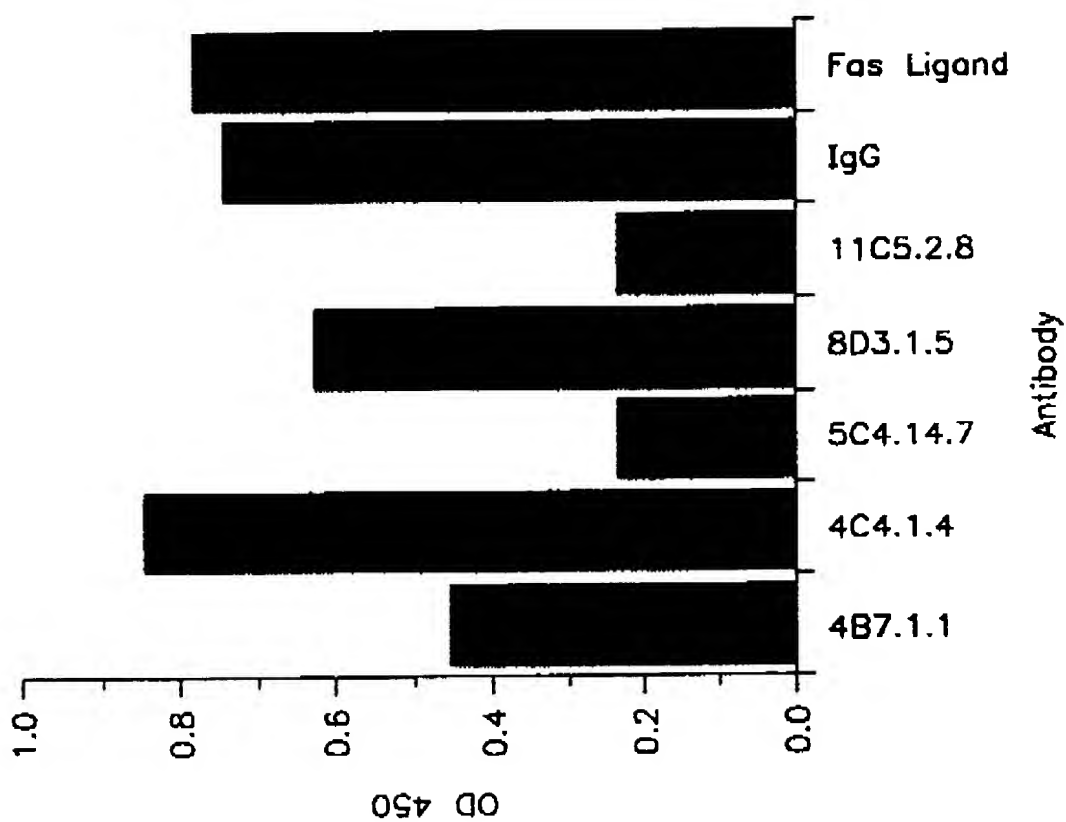


FIG. 14